GENETIC DIVERSITY IN SWEET CORN (*Zea mays* L. *saccharata*) CULTIVARS EVALUATED BY AGRONOMIC TRAITS

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ABSTRACT

That is why custodians of gene banks characterize their resources, noting the selected traits of consent. In this study, diversity among 11 sweet corn cultivars was studied in Erzurum, Turkey during the 2017 cropping season to characterize them based on agronomic capacity, twenty two traits were analysed using correlation and regression analysis, Principle Component Analyses (PCA) and cluster analysis. The results showed positive and significant correlation of the yield of marketable ear (YME) with ear diameter (ED) and the number of marketable ears (NME) whereas negatively and significantly correlated with the 1000 kernel weight (TKW). Fresh kernel yield (FKY) was positive and highly significantly correlated with the ear yield (EY), ear length (EL), number of kernels per row (NK/R) and the number of kernels per ear (NK/E) while it was negative and highly significantly correlated with plant height (PH), first ear height (FEH), ear weight (EW) and the number of kernel rows per ear (NKR/E). Total soluble solids (TSS) content showed negative and significant correlation with green mass yield (GMY) and (NK/R). Stepwise regression showed that an increase of (TKW) traits leads to the reduction of the (YME) and (FKY). The minimum and maximum heritability observed from the traits moisture content (7.69%) and first ear height (95.82%), in this study (YME) and (FKY) heritability was 88.76 and 85.24%, respectively. For better understanding of the relationships, similarities and dissimilarities among the morphological and agronomic trait indicators of 11 genotypes, a principal component analysis was used. The first, second, third and fourth principal components explained, respectively, 37.92, 22.70, 15.61 and 12.03% of the total variance in all traits. Cluster analysis based on traits classified the genotypes into four groups. Cluster I consisted of (Kompozit Seker and BATE Tatli varieties), cluster I consisted of (Overland, Baron F₁, SHY1036 and Febris varieties), cluster III (Signet variety), cluster IV (Tanem F1-Challenger-Khan F1-Argos varieties), respectively.

Key words: ***Cluster analysis, Genetic diversity and Heritability, PCA, Regression, Sweet corn.***

INTRODUCTION

Sweet corn (*Zea mays* L. var *saccharata*), which realized as a vegetable, is a special type of corn with particular properties, such as sweet taste, thin pericarp and endosperm with a soft texture, and a high nutritional value (Kwiatkowski and Clemente 2007). It is meant only for human consumption, in novel form or in processed foods (Teixeira *et al* 2001). In Turkey, there is no data about sweet corn yield and production, but an estimated production area of 1-2% from the total production area of the corn crop (Arslan and Williams 2015).

Kernel yield is the most important agronomic traits of corn, that is why, most of its breeders are highly treated. Additionally, the attention should be paid to the quality of the kernel itself (Sreckov *et al* 2007). The grain yield of fresh corn is a quantitative character and dependent on its own component parts. Crop breeders commonly prefer yield components that

indirectly increase yield. Indirect selection of yield components can increase grain yield. Therefore, it is important to know the relationships among yield traits in sweet corn to create higher yields (Kashiani and Saleh 2010). To accomplish this purpose, selection of superior and high yielding varieties is really substantial. Referable to the increasing of sweet corn demand and utilization of commodities and services, its improvement is an important matter. Approximation of the genetic distance is one of appropriate tools for parental selection of sweet corn hybridization programs. Appropriate selection of the parents is important in crossing nurseries to get up the genetic recombination for potential yield increase (Islam 2004). The logical orientation of genotypes under the influence of agronomic traits can be applied as an effective tool for rapid selection of high and early maturing varieties. Counting at the significant adaptation with the common method can providing a clear view of the strength of the genotype (Mohammed *et al* 2015). Theoretically, a characteristic is a desirable criterion for selection of yield breeding programs which has a high correlation with yield and heritability (Khorasani *et al* 1997). Correlation of specific feature with other features lending to grain yield is crucial for indirect selection of genotypes for higher grain yield (Kumar *et al* 2010). Different researches have been taken for determining the phenotypic and genotypic correlation between important agronomic traits and corn production. However choices based on simple correlation only without the interactions among yield components may mislead the breeders to reach their primary goals (Kaya *et al.*2009). The relationships between morphological and agronomic traits have been set up in some crops (Mishra and Subrahmanyam 1973). The genotypes were evaluated using stepwise regression to know which parameter (s) delivers the optimal values for each genotype or group of genotypes (Al-Naggar *et al* 2015). The study of genetic diversity with suitable measurements like genetic coefficient of variance and heritability evaluations are essential to have an applicable training program (Al-Tabbal and Al-Fraihat 2012). It has been being shown that heritability is in the broad and narrow sense and can be illustrated on the foundation of single plants and entry means (Smalley *et al.*2004). Magorokosho *et al* (2003) reported that with enhancement of water stress maize grain yield reduced. Maize displays more variation of phenotypes than any other grain crop (Mahmood *et al* 2004). Chaudhary (2001) establish that the genotype coefficient of variation (GCV) is not an

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absolute mean to know the heritable diversity present and should be taken together with heritability evaluations. The primary aim of this study was to screen the sweet corn based on agronomical traits and capture the potential genetic diversity among the genotypes.

MATERIALS AND METHODS

Plant material and experimental design

Seeds of eleven sweet corn genotypes (Table 1) were sown in a randomized complete block design (RCBD) with three replications under Erzurum/Turkey conditions. The experimentation was directed at the Experimental Farm of Atatürk University, Faculty of Agriculture, Erzurum/Turkey during 2017 cropping season. During the experiment period the monthly minimum and maximum temperature were -1.1 and 27.4°C respectively. Thus minimum and maximum average monthly rainfall was 6.4 and 59.0 millimetres.

Measurement of parameters

At field maturity, samples of 11 sweet corn genotypes after omitting marginal effects, ten plant samples were selected indiscriminately. Different agronomic traits were evaluated such as: silking period (SP), harvesting period (HP) Asabe (2008), moisture content (MC%), number of tillers/plant (NT), number of plants/ha (NP/ha), plant height (PH, cm), first ear height (FEH, cm), number of leaves/plant (NP), number of ears/plant NE, green mass yield kg/ha (GMY), ear yield kg/ha (EY), Ear weight (EW, g), ear length (EL, cm), ear diameter (ED, mm), number of marketable ear/ha (NME), number of kernel rows per ear (NKR/E), number of kernels per row (NK/R), number of kernels per ear (NK/E), fresh kernel yield kg/ha (FKY), 1000 kernels weight (TKW, g) and total soluble solids (TSS) content (%) during harvest time (Esiyok ve Bozokalfa 2005).

Statistical analysis

Evaluations of the cluster analysis were based on world's method using squared Euclidian distance (Kumar *et al* 2010) and identify the cutting point using discriminate analysis. Correlation, PCA and stepwise regression analysis were performed using SPSS version 20.0 computer program. Based on mathematical expectation, genotypic and phenotypic variance mean squares and heritability were estimated and buy below equations their

Table 1. The list of sweet corn genotypes used in this study.

No.	Genotype name	Specifications
1	Argos	Super sweet, maturity period 80-90 day, kernel colour golden yellow, tolerance to transportation
2	Baron F_1	Super sweet, very early variety, high yielding, plant height 190-195 cm, first ear height 60 - 65 cm, ear length 19,9 cm, ear diameter 5,3 cm, number of kernel rows per ear 16-18, unhusked ear weight 330-335 g, kernel colour dark yellow, tolerance to lodging, tolerance to transportation
3	BATEM Tatlı	Standard sweet corn, maturity period 70-80 day, total soluble sugar content 13.8-15.3%, crude protein content 13.7-13.9%
4	Challenger	Super sweet, maturity period 80-85 day, high sugar content, kernel colour yellow, plant height 170-180 cm
5	Febris	Super sweet, maturity period 87 days, ear length 16-18 cm, tolerance to lodging, moderate plant height
6	Khan F_1	Super sweet, early variety, high yielding, plant height 190-200 cm, first ear height 50 - 60 cm, ear length 22-23 cm, ear diameter 5-5,2 cm, number of kernel rows per ear 16-18, unhusked ear weight 340-350 g, kernel colour dark yellow, tolerance to lodging, tolerance to transportation
7	Kompozit Şeker	Standard sweet corn, maturity period 77-84 day, plant height 80- 220 cm, fresh ear yield 12500–21000 kg/ha, kernel colour yellowish orange
8	Overland	Standard sweet corn, days to flowering 65-69 day, plant height 200-220 cm, first ear height 110 cm, ear length 16-20 cm, number of kernel rows per ear 18-20, kernel colour white, ear yield 8500-10500 kg/ha, sugar k 3.8%, protein content 11.3%
9	SHY1036	Super sweet, tolerance to diseases, maturity period 100-110 day, high sugar content, kernel colour yellow, plant height 210-220 cm
10	Signet	Sugary enhanced, maturity period 60-65 day, very high sugar content, kernel colour yellow, plant height 150-160 cm
11	Tanem F_1	Standard sweet, early maturity, plant height 170-180 cm, first ear height 45-60 cm, ear length 20-22 cm, ear diameter 4,5-5 cm, number of kernel rows per ear 16-18, ear weight 460-480 g, kernel colour yellow

Coefficient variation were calculated as follows:

1. $V_E = MS_e$

2. $V_G = \dfrac{MS_g - MS_e}{r}$

3. $V_P = V_G + V_E$

4. $\% \, PCV = \dfrac{\sqrt{V_P}}{\bar{x}} \times 100$

5. $\% \, GCV = \dfrac{\sqrt{V_G}}{\bar{x}} \times 100$

6. $\% \, H_b = \dfrac{V_G}{V_P} \times 100$

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In which V_E is environmental variance, MS_e and MS_g are the mean squares of the error and genotypes, respectively, V_p is phenotypic variance, V_G is genotypic variance, PCV and GCV are phenotypic and genotypic coefficient of variation, respectively, and $\overline{X}$ is mean of parameter in the experiment. H_b is the heritability in the sorghum (Bhagasara *et al* 2017).

RESULTS AND DISCUSSION

Correlation

In this study the correlation analysis was done based on yield of marketable ear (YME), fresh kernel yield (FKY) and total soluble solids (TSS) content. The results showed that (YME) was positive and significantly correlated with ED (r = 0.579*) and NME(r = 0.882**), whereas it was negatively and significantly correlated with TKW (r = 0.690*). Fresh kernel yield showed a positive and highly significant correlation with EY (r = 0.882**), EL (0.r=0.981**), NK/R (r = 0.891**) and NK/E (r = 0.980) while it showed negative and highly significant correlation with PH (r = 0.930**), FEH (r = 0.818**), EW (r = 0.838**) and NKR/E (r = 0.692*). In case of total soluble sugar content; the results showed a negative and significant correlation with GY (r = 0.617*) and NK/R (r = 0.609*).

Rezaei and Ramezani (2010) reported that the number of kernel rows per ear were positively correlated with number of kernels per ear (r = 0.77**) (Alaei 2012) and negatively correlated with 1000 kernel weight (r = 0.69*) (Hefny 2011). The same result was observed on a number of kernels per row was correlated positively with the number of kernels per ear (r = 0.78**) and negatively correlated with 1000 kernel weight (r = 0.67*). The number of marketable ears, number of kernels per row and number of kernels per ear had a positive correlation with the yield of marketable ears (Kashiani *et al* 2010, Liu 2009, Wang *et al* 1999, Xie *et al* 2010 and Yousuf and Saleem 2001). The fresh kernel yield of sweet corn can be improved by selection of high era weight, ear length, yield of marketable ears, and a number of marketable ears (Has and Has 2009).

Rahman *et al* (2015) stated that the correlation is also an important measurement indicating that traits which should be given importance to increase yield. They also reported that two associations revealed a positive significant correlation: plant height with yield/plant and ear diameter with ear length.

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Table 2. Correlation coefficients among different morphological and agronomic traits of sweet corn under Erzurum conditions.

	SP	HP	MC	NT	NP	PH	FEH	LN	NE	GMY	EY	EW	EL	ED	YME	NME	NKR/E	NK/R	NK/E	FKY	TKW
HP	0.949**																				
MC	0.23	0.40																			
NT	-.694*	-.679*	-0.05																		
NP	-0.01	-0.04	-0.41	-0.07																	
PH	0.47	0.31	-0.19	-0.37	0.33																
FEH	0.738**	0.597*	0.14	-0.48	0.20	0.789**															
LN	0.646*	0.661*	0.26	0.716**	-0.09	0.40	.652*														
NE	-0.723**	-0.733**	0.14	0.40	0.12	0.27	0.50	-0.633*													
GMY	-0.32	-0.31	0.16	-0.11	0.45	-0.52	-.597*	-0.35	.605*												
EY	-0.29	-0.14	0.18	0.19	-0.39	-0.709	-0.584	-0.21	0.26	0.44											
EW	0.799**	0.678*	0.06	-0.57	0.27	0.871**	0.959**	0.643*	-0.54	-0.580*	-0.587*										
EL	-0.34	-0.15	0.24	0.29	-0.39	-0.888**	-0.766**	-0.35	0.21	0.48	0.916**	-0.761**									
ED	0.25	0.34	0.04	-0.52	0.47	0.34	-0.21	0.36	-0.08	.583*	0.23	-0.17	0.32								
YME	0.26	0.29	0.48	-0.24	-0.21	-0.25	0.12	0.22	-0.04	0.08	0.579*	0.06	0.41	-0.01							
NME	0.35	0.45	0.25	-0.57	-0.50	0.42	-0.12	0.42	-0.09	0.55	0.48	-0.11	0.47	0.882**	0.46						
NKR/E	0.723**	0.659*	-0.11	0.845**	0.28	0.631*	0.629*	0.604*	-0.55	-0.17	0.585*	0.738**	-0.611*	0.26	-0.18	0.15					
NK/R	-0.47	-0.33	0.03	0.15	-0.40	0.767	0.840	-0.45	0.55	0.815**	0.814**	-0.795	0.864**	0.43	0.27	0.50	-0.50				
NK/E	-0.40	-0.23	0.20	0.25	-0.45	0.891**	-0.797**	-0.39	0.35	0.632*	0.911**	-0.801**	0.980**	0.36	0.41	0.51	-.605*	.933**			
FKY	-0.45	-0.27	0.20	0.35	-0.40	0.930**	0.818**	-0.42	0.35	0.55	0.882**	0.838**	.981**	0.33	0.37	0.46	-0.692*	0.891**	0.980**		
TKW	-0.54	-0.595*	-0.13	0.710**	0.41	0.13	-0.05	0.52	0.45	-0.35	-0.35	-0.13	-0.30	-0.690*	0.37	-0.778**	0.46	-0.29	-0.32	-0.18	
TSSC	0.15	0.01	-0.24	0.21	0.50	0.17	0.32	-0.04	0.52	-0.617*	-0.41	0.24	-0.34	0.56	-0.08	-0.54	0.08	-0.609*	0.42	-0.37	0.29

Note: * : significant at P ≤ 0.05; ** : significant at P ≤ 0.01; SP: silking period; HP: harvesting period; MC: moisture content; NT: number of tillers per plant; NP: number of plants/ha; PH: plant height; FEH: first ear height; LN: number of leaf per plant; NE: number of ears per plant; GMY: green mass yield kg/ha; EY: ear yield kg/ha; EW: ear weight; EL: ear length; ED: ear diameter; YME: yield of marketable ear kg/ha; NME: number of marketable ear/ha; NKR/E: number of kernel rows per ear; NK/R: number of kernel per row; NK/E: number of kernels per ear; FKY: fresh kernel yield kg/ha; TKW: 1000 kernels weight and TSS: total soluble solids content.

The positive and significant correlation between plant height and yield/plant had also been recorded by Salami *et al* (2007) and Rafiq *et al.* (2010). This positive and significant association between the traits suggested additive genetic model, thereby less affected by the environmental fluctuation. Besides, most of the associations were recorded as positive but non-significant. This type of association referred information about the inherent relation among the pairs of combination. The positive and nonsignificant association between plant height with ear height and ear height with grain yield had also been observed by Olakojo and Olaoye (2011).

Munawar *et al* (2013) also studied positive, non-significant association between plant height with ear height and ear length. Positive and non-significant association for ear height with ear length and yield/plant was recorded by Rafiq *et al* (2010). The negative insignificant association for number of kernels/ear with 1000-kernel weight referred a complex linke of relation among the pair of combinations.

Regression analyses

Stepwise regression was used to remove the effects of ineffective or low impact on yield traits in the regression model. The results of the stepwise regression that with the input of FKY, TKW, EY and NKR/E the model results in 96.1, 1.8, 1.0 and 0.8, respectively with the total of 99.7 variants. From the same results, NKR/E and TKW referred to the YME negatively, which means that an increase of these two traits leads to the decrease of the EY and FKY. Khazaei *et al* (2010) in his study of correlation, regression and path coefficient analysis on sweet corn (*Zea mays* var. *saccharata*) reported that, the results of regression analysis for grain yield showed that grain number and 1000 grain weight accounted for 98% of the grain yield variation. Based on this study inference can be drawn that higher fresh kernel yield improvement may be achieved by the selection of ear weight, ear length, yield of marketable ears and a number of marketable ears (Kumar *et al* 2015).

Table 3. Regression analyses for some targeted traits.

Model	Level	Independ variable	Width of Origin	Coefficients	F	Explanation factor minor	Explanation factor Model (cumulative)
Y1	Y1	FKY	673.11	1.44	219.16**	96.1	96.1
	Y1	FKY	673.11	1.4	219.16**	96.1	96.1
Y2	Y2	TKW	10987.6	-31.43	189.24**	1.8	97.9
	Y1	FKY	673.11	1.11	219.16**	96.1	96.1
Y3	Y2	TKW	10987.6	-24.83	189.24**	1.8	97.9
	Y3	EY	4577.78	0.43	209.20**	1	98.9
Y4	Y1	FKY	673.11	1.1	219.16**	96.1	96.1
	Y2	TKW	10987.6	-42.69	189.24**	1.8	97.9
	Y3	EY	4577.78	0.5	209.20**	1	98.9
	Y3	NKR/E	16762.4	-443.66	458.13**	0.8	99.7
Y1 = 673.11 + 1.44 (X1)							
Y2= 10987.56+ 1.40 (X1) -31.436 (X2)							
Y3 = 4577.78 + 1.11 (X1) -24.83 (X2) - 0.43 (X3)							
Y4 = 16762.37+ 1.10 (X1) -42.69 (X2) - 0.50 (X3) -443.66 (X4)							

Note: F: significance, **: significant at 0.01 probability level

Heritability

The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Al-Tabbal and Al-Fraihat 2012).

For the measured traits in this study, genetic parameters such as genotypic and phenotypic coefficient of variation as well as heritability were computed (Table 4). In all traits, PCV was higher than GCV values are close to the findings that were reported by Salami *et al.* (2007), Bello *et al.* (2012), Anshuman *et al.* (2013) and Rahman *et al.* (2015); which means the effect environmental factors was indicated in all the traits. Minimum and maximum GCV was observed on the number of kernel rows per ear (0.002%) and the yield of marketable ears (5150.09%) traits. The estimates of the genotypic coefficient of variation (GCV) reflect the total amount of genotypic variability. Since most of the economic characters (grain yield) are complex in inheritance and are greatly influenced by several genes interacting with various environmental conditions, the study of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV)

is not only useful for comparing the relative amount of phenotypic and genotypic variations among different traits but also very useful to estimate the scope for improvement by selection.

The maximum and minimum heritability was observed from the traits moisture content (7.69%) and first ear height (95.82%); in this study yield of marketable ears (YME) and fresh kernel yield (FKY) heritability was 88.76% and 85.24%, respectively. Heritability estimates are of tremendous significance to the breeder, as its magnitude indicates the accuracy with which a genotype can be recognized by its phenotypic expression. In traits with high heritability, the effect of the genetic variance was greater than the environmental variance and hence the selection of genotypes in the early generations based on these traits will be reliable and successful.

Table 4. Minimum value (Min), maximum value (Max), coefficient of genotypic variation (GCV), coefficient of phenotypic variation (PCV), heritability (Hb) for the studied traits in sweet corn.

Traits	Min	Max	PCV%	GCV%	Hb (%)
Silking period (day)	75.70	90.30	4.91	4.36	78.95
Harvest period (day)	104.70	120.30	4.10	3.42	69.84
Moisture content (%)	71.80	73.70	1.51	0.42	7.69
Nunmber of tillers per plant	0.00	1.84	74.05	48.58	43.04
Nunmber of plants/ha	6500.00	7833.30	7.75	4.23	29.80
Plant height (cm)	181.60	218.40	7.09	5.34	56.79
First Ear Height (cm)	42.50	89.20	19.66	19.25	95.82
Number of leaves/plant	7.67	9.80	11.22	6.48	33.33
Number of ears/plant	0.93	1.33	11.16	8.95	64.29
Green Mass Yield (kg/ha)	3301.70	5025.80	251.10	200.01	63.45
Eea Yield (kg/ha)	1171.90	186.80	1537.69	1292.01	70.60
Ear weight (g)	240.10	273.20	2.37	2.01	72.34
Ear length (cm)	16.20	19.30	0.06	0.05	81.17
Ear diameter (mm)	42.60	50.90	3185.14	3093.77	94.35
Yield of marketable ear (kg/ha)	1030.40	1619.10	5466.31	5150.09	88.76
Number of marketable earsha	1277.80	7166.70	7.44	4.78	41.31
Number of kernel rows per ear	14.50	19.40	0.0035	0.0031	80.92
Numner of kernels per row	33.30	39.10	0.022	0.020	80.71
Number of kernels per ear	520.00	696.70	0.70	0.63	81.98
Fresh kernel yield (kg/ha)	114.30	1171.90	4.15	3.83	85.24
1000 kernels weight (g)	288.20	356.60	8.06	6.03	56.00
Total soluble solids (%)	13.80	22.30	17.71	16.88	90.82

On the contrary, for traits with low heritability, the effect of environmental variance was high and most phenotypic changes was caused by environmental effects, and the choice of genotypes should continue for the next generations. Our finding was supported by Winnows *et al* (2010) who found that heritability was reported high for ear height, ear diameter, 100-kernel weight and grain yield. Aminu and Izge (2012) studied high heritability for plant height and yield/plant. Very high heritability was observed for plant height, ear height, number of kernels/ear, 1000-kernel weight and yield/plant by Bello *et al* (2012) and Anshuman *et al* (2013). Has and Has (2009) reported that ear length, row no/ear, number of branches/tassel and silking data had high heritability value. Meanwhile, ear weight, husk weight, kernel depth and cob diameter had moderate to low heritability value. Plant height was recorded as the most heritable trait (96.7%), days to tasseling (77.3%) and ear length (72.4 cm). Yield of marketable ears was recorded as the most heritable trait (0.99**), days to tasseling (77.3%) and number of marketable ears (0.98**).

Principal component analysis

The role of the principal components analysis is to get a low number of linear combinations, which account for most of the variability in using information. In this work, the four components have been taken out, since four components had eigenvalues greater than or equal to one. The first principal component alone contributed 44.31 % of the total variation, while the second principal components accounted for 26.17 % of the total variation, the third principal component alone contributed 10.10 % of the total variation, and the fourth principal component alone contributed 6.19 % of the total variation Table 5. The first four principal components explained 86.76 percent of the total variation across the 11 sweet corn accessions for the twenty two traits studied (Table 5).

To get better knowledge about the relationship among all genotypes principal component analysis (PCA) was executed to discover diverse genotypes for successful hybridization program (Tarighaleslami *et al* 2012). Mohammed *et al* (2015) as sweet potato accessions (116) grown under rainfed conditions and Mushtaq *et al* (2016) from his study on maize reported that PCA abridged the total variation into four principle components.

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Table 5. Principal Components Analysis of sweet corn (*Zea maize* L.) genotypes.

| Component Number	Component name	Eigenvalue	Percentage of Variance	Cumulative Percentage
1	Silking period (day)	9.75	44.31	44.31
2	Harvest period (day)	5.76	26.17	70.47
3	Moisture content (%)	2.22	10.10	80.58
4	Number of tillers/plant	1.36	6.19	86.76
5	Number of pants/ha	0.99	4.53	91.29
6	Plant height (cm)	0.58	2.63	93.92
7	First ear height (cm)	0.51	2.31	96.23
8	Number of leaves/plant	0.44	1.98	98.21
9	Number of ears/plant	0.33	1.48	99.69
10	Green mass yield/ha	0.07	0.31	100.00
11	Ear yield/ha	0.00	0.00	100.00
12	Ear weight (g)	0.00	0.00	100.00
13	Ear length (cm)	0.00	0.00	100.00
14	Ear diameter (mm)	0.00	0.00	100.00
15	Yield of marketable ear/ha	0.00	0.00	100.00
16	Number of marketable ears/ha	0.00	0.00	100.00
17	Number of kernel rows/ear	0.00	0.00	100.00
18	Number of kernels/row	0.00	0.00	100.00
19	Number of kernels/ear	0.00	0.00	100.00
20	Fresh kernel yield/ha	0.00	0.00	100.00
21	1000 kernels weight (g)	0.00	0.00	100.00
22	Total soluble solids (%)	0.00	0.00	100.00
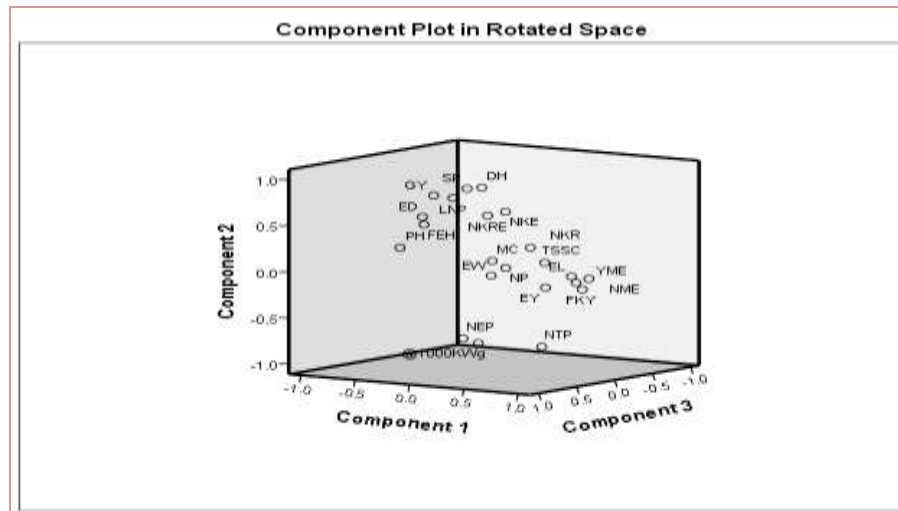
Fig. 1. Biplot analysis of selection traits estimated under Erzurum conditions based on the PC₁ (43.12%), PC₂ (24.13%), PC₃ (10.14%) and PC₄ (7.79%) for 11 genotypes of sweet corn.

Table 6 shows the weight of each trait component. The trait that contributed most positively to PC1 was YME and NME (0.96), FKY (0.93), EY (0.87), EL (0.86), EW (0.67), NK/E (0.58), NKR (0.57), NKR/E (0.34), ED (0.25), and NT/P (0.20) whereas PH, FEH, TKW, GY, PD and LN/P, TSSC and NE/P were negatively correlated with PC1. Our results are supported with those of Disasa *et al* (2017). In their study on sweet sorghum (*Sorghum bicolor*) demonstrated that fresh grain yield and total soluble sugar content respectively were positively and negatively contributed in the PC1. The PC2 had 24.13 % of the total variance. The MP (0.83), SP (0.81), GY (0.77), LN/P (0.73), NKR/E (0.61), NK/E (0.52), FEH (0.42), PH (0.20), NK/R (0.19), MC (0.13) and ED (0.09) have positive contribution, whereas the rest of the traits were negatively correlated with the PC2. This was reinforced by the study of Latif *et al* (2015) and Disasa *et al* (2017) on sixty cotton (*Gossypium hirsutum* L.) genotypes and sweet sorghum (*Sorghum bicolor*), who found positive contribution of ear diameter and plant height in the first component, while the rest of the traits had negative contribution.

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Table 6. Component weights for the evaluated traits.

Weights	Ear length	Harvesting period	Green yield	Moisture content
Silking period (day)	-0.39	0.79	-0.21	0.26
Harvest period (day)	-0.24	0.82	-0.18	0.35
Moisture content (%)	0.04	0.08	0.08	0.85
Number tillers/P	0.30	-0.86	-0.21	0.04
Number of plant/ha	-0.27	-0.11	-0.55	-0.43
Plant height (cm)	-0.93	0.11	-0.09	-0.06
First ear height (cm)	-0.82	0.35	-0.25	0.29
Number of leaves/plant	-0.40	0.71	-0.03	0.28
Number of ears/plant	0.17	-0.66	0.65	-0.10
Green mass yield/ha	0.50	0.07	0.75	-0.27
Ear yield/ha	0.84	0.01	0.18	0.33
Ear weight (g)	-0.82	0.43	-0.23	0.19
Ear length (cm)	0.96	-0.01	0.12	0.22
Ear diameter (mm)	0.32	0.67	0.53	-0.15
Yield of marketable ear/ha	0.31	0.24	-0.04	0.71
Number of ears/ha	0.42	0.71	0.45	0.20
Number of kernel rows/ear	-0.58	0.72	-0.03	-0.26
Number of kernels/row	0.83	-0.06	0.51	-0.03
Number of kernels/ear	0.94	-0.03	0.27	0.17
Fresh kernel yield/ha	0.95	-0.11	0.20	0.17
1000 kernels weight (g)	-0.28	-0.88	-0.19	-0.08
Total soluble solids (%)	-0.16	-0.09	-0.89	-0.16

Positive and significant correlation between plant height and yield per plant had also been reported by Mushtaq *et al* (2016) and Disasa *et al* (2017). The PC3 having positive correlations with ED (0.87), NE/P (0.77),

NKR/E (0.63), ED (0.58), NK/E (0.43), EY (0.42), FKY (0.22), YME (0.20), MC (0.13), NME (0.10), EL (0.09) and NK/R (0.04), while Mushtaq *et al* (2016) stated that there is a positive contribution of PC3 with ear diameter, whereas the other traits were negatively correlated with PC3 Mushtaq *et al* (2016) and Disasa *et al* (2017). In case of PC4 a positive contribution was proved with MC (0.86), NK/R (0.68), NK/E (0.34), HP and LN/P (0.31), FEH and NE/P (0.25), EL (0.24), SP (0.22), NME (0.19), FKY (0.11), YME (0.09), NT/P (0.08) and TKW (0.01) (Mushtaq *et al* 2016 and Disasa *et al* 2017), while the other traits were negatively correlated with PC4 (Table 6). The positive contribution of PC4 to first ear height was observed on maize, while the negative contribution was found with 1000 kernels with on the study results of Mushtaq *et al* (2016) and Disasa *et al* (2017) on maize and sweet sorghum (*Sorghum bicolor*) respectively. Mushtaq *et al* (2016), reported that the first principal component accounted the maximum portion (83.364%) of total variance, and characters that contribute more positively to this component is plant height, ear height, days to 50% silking, ear length, grain yield per plant, grain yield and shelling%. The second component, which featured ear height as the principal trait, explained an additional 8.276% of the phenotypic variation. Finally, third and fourth principal component; contributed around 3.762% and 2.527%, respectively, of the variability present among the accessions for the traits used in this study. The third principle component explained the pattern of variation in 100 grain weight, and for fourth principle component, the maximum variation is contributed by days to 50% silking; these outcomes are supporting our findings.

Cluster analysis

The phenotypic characterization was used in the cluster analysis to determine whether homogenous groups are formed by relatedness and to what extent, and whether gained results were in accordance with the pedigree of observed sweet maize inbreds. Therefore, the results of the cluster analysis can be beneficial for the selection of genotypes for further crosses (Babic *et al* 2010). Eventually, the genotypes are grouped in four major clusters I (18.18%), II (36.36%), III (9.09%) and IV (36.36%). Our results reinforced by Rahman *et al* (2015), and Subramanian and Subbaraman (2010) whom worked on maize diversity which results also in four clusters.

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Cluster I was the largest cluster and cluster II has two genotypes only. Cluster I is further divided into two clusters (I_1 and I_2) in which cluster I_1 contained the genotype Kompozit Seker, whereas cluster I_2 consisted of BATEM Tatlıgenotype, cluster II also is divided into two sub-clusters; cluster II_1 and II_2, cluster II_1 consisted of Overland and Baron genotypes, whereby cluster II_2 contained SHY1036 and Febris genotypes, while cluster III consisted of Signet genotype. Cluster IV was divided into two sub-clusters; cluster IV_1 which contained Tanem F_1 genotype, whereas cluster IV_2 consist of three genotypes; Challenger, Khan F_1, and Argos. By incising the dendrogram, the genotypes categorized into four groups. Using discriminant analysis revealed that 100% of the members constituted four groups (Mhoswa *et al.* 2016). The highest genetic distance was shown between Argos and Kompozit genotypes.
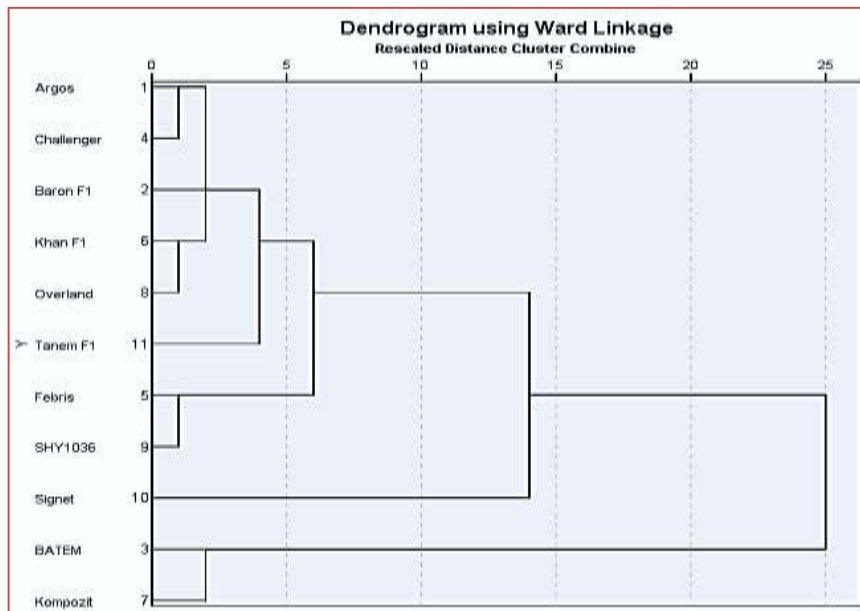

Fig. 2. Tree diagram of 11 genotypes for 22 studied variables using hierarchical cluster analysis (ward's method and squared Euclidean distance).

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CONCLUSIONS

In the present study both cluster analysis and PCA could effectively discriminate the accessions of sweet corn cultivars with different agronomical traits. Thus, it can be inferred that phenotypic attributes do have an important role in genetics and breeding studies. Grouping a large number of germplasm accessions into few numbers of homogenous clusters facilitates the selection of diverse parents for crossing programs. This study has revealed the existence of adequate genetic variability in the material studied. This knowledge could be crucial in enhancing the efficiency of maize breeding programs in Turkey. This genetic diversity and the strong genetic association between grain yield and the agronomic traits would aid in indirect selection thus helping the breeders in the development of composites and synthetics for the resource constraint farmers with limited access to hybrid seeds. In addition, the correlation of the highly heritable traits with complex ones could help determine whether selection for one trait has any effect on another. Ear diameter and ear yield traits which showed the highest genotypic coefficient variability, high broad sense heritability estimates, and had strong positive association with yield of marketable ear can be used as effective selection indices for grain yield improvement.

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GENETIC DIVERSITY IN SWEET CORN (*Zea mays* L. *saccharata*) CULTIVARS EVALUATED BY AGRONOMIC TRAITS

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تم إجراء هذا البحث في كلية الزراعة – جامعة اتاتورك – ارضرروم بتركيا خلال الموسم ٢٠١٧ , حيث تم استخدام ١١ صنف من الذرة السكرية في هذه الدراسة وتم إجراء تحليل التباين وتحليل الارتباط والانحدار والتحليل العنقودي وتحليل المكونات (PCA) للصفات المدروسة. أظهرت نتائج الدراسة ان هناك ارتباطاً موجباً ومعنوياً بين صفة انتاجية الكوز القابل للتسويق (YME) وكلاً من قطر الكوز (ED) وعدد الكيزان القابلة للتسويق (NME), بينما كان الارتباط سالباً ومعنويا لصفة وزن الألف حبة (TKW). أما بالنسبة لانتاجية الحبوب الطازجة (FKY) كان الارتباط موجبا ومعنويا مع كل من الصفات التالية انتاجية الكيزان (EY), طول الكوز (EL) , عدد الحبوب في الصف (NK/R) , عدد الحبوب في الكوز (NK/E) وكان الارتباط سالبا ومعنويا مع صفة طول النبات (PH) وارتفاع أول كوز (FEH) ووزن الكوز (EW) وعدد صفوف الحبوب بالكوز (NKR/E) بينما كان الارتباط سالبا ومعنويا بين صفة المحتوى الاجمالي للمواد القابلة للذوبان (TSS) وكلا من انتاجية الجزء العلفي (GMY) وعدد الحبوب في الصف (NK/R) . وأظهر نتائج تحليل الانحدار ان زيادة (TKW) أدى إلى انخفاض انتاجية الكيزان القابل للتسويق (YME) وانتاجية الحبوب الطازجة (FKY) اما بالنسبة لنسبة التوريث فقد اظهرت نتائج الدراسة ان نسبة التوريث بالنسبة لصفة ارتفاع اول كوز FEH (٩٥,٨٢) , وصفة قطر الكوز ED (٩٤,٣٥) وبالنسبة لصفة المحتوى الاجمالي للمواد القابلة للذوبان TSS (٩٠,٨٢) كانت الأعلى أما بالنسبة لصفة نسبة الرطوبة في الحبوب MC (٧,٦٩) وعدد النباتات في الهكتار NP/ha (٢٩,٨٠) وصفة عدد الاوراق في النبات NL (٣٣,٣٣) كانت الاقل. كما تم استخدام تحليل المكونات الرئيسية لفهم العلاقة واوجه التشابه مابين الصفات الزراعية والصفات المورفولوجية للنبات واظهرت النتائج ان قيمة المكونات الرئيسية الأربعة ٣٧,٩٢ , ٢٢,٧٠ , ١٥,٦١ , ١٢,٠٣ % على التوالي . وللتمييز مابين الاصناف المستخدمة في الدراسة تم إجراء التحليل العنقودي للصفات المدروسة وأظهرت نتائج التحليل وجود اربع مجموعات من الأصناف وهي المجموعة الأولى (Kompozit Seker و MATEM Ttalı) المجموعة الثانية (Overland-Baron F₁-SHY1036-Febris) والمجموعة الثالثة (Signet) المجموعة الرابعة (Tanem F₁-Challenger-Khan F₁-Argos) على التوالي .